AMENDMENTS TO THE SPECIFICATION

Please amend paragraph numbers [0054] through [0056] at pages 11-12 to read as follows:

[0054] Preferably, the RDP58 peptides for use in the compositions and methods disclosed herein comprise oligopeptides having the sequence B-X-X-X-B-X-X-X-J-Tyr (set forth as SEQ ID NO:1), where B is a basic amino acid, preferably Lys or Arg, particularly Arg on at least one position, preferably at both positions; J is Gly, B or an aliphatic hydrophobic amino acid of from 5 to 6 carbon atoms, particularly Gly or B; and X is an aliphatic or aromatic amino acid. In one embodiment, at least three X amino acid residues are the same non-polar aliphatic amino acid, preferably at least four are the same non-polar aliphatic amino acid, more preferably at least five are the same non-polar aliphatic amino acid, and most preferably, all are the same non-polar aliphatic amino acid. In a preferred embodiment, the non-polar aliphatic amino acids are of from 5 to 6 carbon atoms, particularly 6 carbon atoms, particularly the non-polar aliphatic amino acids Val, Ile, Leu, and nL. Thus, in some embodiments, X is any amino acid other than a charged aliphatic amino acid, and preferably any amino acid other than a polar aliphatic amino acid.

[0055] Of the six amino acids indicated by X in the B-X-X-X-B-X-X-X-J-Tyr peptide sequence (set forth as SEQ ID NO:1), preferably at least 3 are aliphatic amino acids of from 5 to 6 carbon atoms, more preferably at least 4 are aliphatic amino acids of from 5 to 6 carbon atoms, most preferably at least 5 are aliphatic amino acids of 5-6 carbon atoms, more particularly 6 carbon atoms. In a preferred embodiment, the aliphatic amino acids are non-polar aliphatic amino acids of from 5 to 6 carbon atoms, particularly Val, Ile, Leu, and nL. The other amino acids may be other uncharged aliphatic amino acids, particularly non-polar aliphatic amino acids or aromatic amino acids.

[0056] Compositions of particular interest will include an RDP58 peptide having the sequence Arg-U-X-X-Arg-X-X-X-J-Tyr (set forth as SEQ ID NO:2), wherein all of the symbols have been defined previously except U, which comprises an uncharged aliphatic amino acid or aromatic amino acid, particularly a non-polar aliphatic amino acid or aromatic amino acid.

Please amend paragraph number [0059] at pages 12-13 to read as follows:

[0059] Exemplary RDP-58 peptides include the following:

bc # (SEQ ID NO)										
1 (SEQ ID NO:3)	Arg	Leu	Leu	Leu	Arg	Leu	Leu	Leu	Gly	Tyr
2 (SEQ ID NO:4)	Arg	Val	Leu	Leu	Arg	Leu	Leu	Leu	Gly	Tyr
3 (SEQ ID NO:5)	Arg	Ile	Leu	Leu	Arg	Leu	Leu	Leu	Gly	Tyr
4 (SEQ ID NO:6)	Arg	Leu	Val	Leu	Arg	Leu	Leu	Leu	Gly	Tyr
5 (SEQ ID NO:7)	Arg	Leu	Ile	Leu	Arg	Leu	Leu	Leu	Gly	Tyr
6 (SEQ ID NO:8)	Arg	Leu	Leu	Val	Arg	Leu	Leu	Leu	Gly	Tyr
7 (SEQ ID NO:9)	Arg	Leu	Leu	Ile	Arg	Leu	Leu	Leu	Gly	Tyr
8 (SEQ ID NO:10)	Arg	Leu	Leu	Leu	Arg	Val	Leu	Leu	Gly	Tyr
9 (SEQ ID NO:11)	Arg	Leu	Leu	Leu	Arg	Ile	Leu	Leu	Gly	Tyr
10 (SEQ ID NO:12)	Arg	Leu	Leu	Leu	Arg	Leu	Val	Leu	Gly	Tyr
11 (SEQ ID NO:13)	Arg	Leu	Leu	Leu	Arg	Leu	Ile	Leu	Gly	Tyr
12 (SEQ ID NO:14)	Arg	Leu	Leu	Leu	Arg	Leu	Leu	Val	Gly	Tyr
13 (SEQ ID NO:15)	Arg	Leu	Leu	Leu	Arg	Leu	Leu	Ile	Gly	Tyr
14 (SEQ ID NO:16)	Arg	Trp	Leu	Leu	Arg	Leu	Leu	Leu	Gly	Tyr
15 (SEQ ID NO:17)	Arg	Leu	Trp	Leu	Arg	Leu	Leu	Leu	Gly	Tyr
16 (SEQ ID NO:18)	Arg	Leu	Leu	Trp	Arg	Leu	Leu	Leu	Gly	Tyr
17 (SEQ ID NO:19)	Arg	Leu	Leu	Leu	Arg	Trp	Leu	Leu	Gly	Tyr
18 (SEQ ID NO:20)	Arg	Leu	Leu	Leu	Arg	Leu	Trp	Leu	Gly	Tyr
19 (SEQ ID NO:21)	Arg	Leu	Leu	Leu	Arg	Leu	Leu	Trp	Gly	Tyr
20 (SEQ ID NO:22)	Arg	Tyr	Leu	Leu	Arg	Leu	Leu	Leu	Gly	Tyr
21 (SEQ ID NO:23)	Arg	Leu	Tyr	Leu	Arg	Leu	Leu	Leu	Gly	Tyr
22 (SEQ ID NO:24)	Arg	Leu	Leu	Tyr	Arg	Leu	Leu	Leu	Gly	Tyr
23 (SEQ ID NO:25)	Arg	Leu	Leu	Leu	Arg	Tyr	Leu	Leu	Gly	Tyr
24 (SEQ ID NO:26)	Arg	Leu	Leu	Leu	Arg	Leu	Tyr	Leu	Gly	Tyr
25 (SEQ ID NO:27)	Arg	Leu	Leu	Leu	Arg	Leu	Leu	Tyr	Gly	Tyr

1nL (SEQ ID NO:28)	Arg	nL	nL	nL	Arg	nL	nL	nL	Gly	Tyr

Please amend paragraph number [0060] at page 13 to read as follows:

[0060] A preferred embodiment of the RDP58 peptide comprises the sequence Arg-nL-nL-nL-Arg-nL-nL-nL-Gly-Tyr (set forth as SEQ ID NO:28), where nL is norleucine and all amino acids other than glycine are the D-stereoisomer.

Please amend paragraph number [0066] at page 15 to read as follows:

[0066] The peptides may also be in the form of oligomers, particularly dimers of the peptides, which may be head to head, tail to tail, or head to tail, there being not more than about 6 repeats of the peptide. The oligomer may contain one or more D-stereoisomer amino acids, up to all of the amino acids. The oligomers may or may not include linker sequences between the peptides. When linker sequences are used, suitable linkers include those comprising uncharged amino acids and (Gly)n, where n is 1-7, Gly-Ser (*e.g.*, $(GS)_n$, $(GSGGS)_n$ (set forth as SEQ ID NO:29), and $(GGGS)_n$ (set forth as SEQ ID NO:30), where n is at least 1), Gly-Ala, Ala-Ser, or other flexible linkers, as known in the art. Linkers of Gly or Gly-Ser may be used since these amino acids are relatively unstructured, which allows interaction of individual peptides with cellular target molecules and limits structural perturbations between peptides of the oligomer. It is to be understood that linkers other than amino acids may be used to construct the oligomeric peptides.

Please amend paragraph number [0082] at pagea 19-20 to read as follows:

[0082] In a further aspect, the presentation sequence confers the ability to bind metal ions to generate a conformationally restricted secondary structure. Thus, for example, C2H2 zinc finger sequences are used. C2H2 sequences have two cysteines and two histidines placed such that a zinc ion is chelated. Zinc finger domains are known to occur independently in multiple zinc-finger peptides to form structurally independent, flexibly linked domains (Nakaseko, Y. et al., *J. Mol. Biol.* 228: 619-636 (1992)). A general consensus sequence is (5 amino acids)-C-(2 to 3 amino acids)-C-(4 to 12 amino acids)-H-(3 amino acids)-H-(5 amino acids) (set forth as SEQ ID NO:31). A preferred example would be -FQCEEC-random peptide of 3 to 20 amino acids-HIRSHTG (set forth as SEQ ID NO:32). Similarly, CCHC boxes having a consensus sequence -C-(2 amino acids)-C-(4 to 20 random peptide)-H-(4 amino acids)-C-(set forth as SEQ ID NO:33) can be used, (Bavoso, A. et al., *Biochem. Biophys. Res. Commun.* 242: 385-389 (1998)). Other examples include (1) -VKCFNC-4 to 20 random amino acids-HTARNCR- (set forth as SEQ ID NO:34), based on the nucleocapsid protein P2; (2) a sequence modified from that of the naturally

occurring zinc-binding peptide of the Lasp-1 LIM domain (Hammarstrom, A. et al., *Biochemistry* 35: 12723-32 (1996)); and (3) -MNPNCARCG-4 to 20 random amino acids-HKACF-(set forth as SEQ ID NO:35), based on the NMR structural ensemble 1ZFP (Hammarstrom et al., *supra*).